



Seq ID	Accession	Length	Score	Match	Sequence	Applicant
19	947	63.0	1506	3	US-10-278-942-1	Sequence 1, Appli
20	947	63.0	1506	3	US-10-694-352-1	Sequence 1, Appli
21	934.8	62.2	1518	2	US-08-114-695A-6	Sequence 6, Appli
22	933.4	62.1	1485	2	US-08-299-810A-27	Sequence 27, Appl
c 23	931.4	62.0	269223	3	US-09-596-002-41	Sequence 41, Appl
24	918	61.1	1540	3	US-09-228-184-1	Sequence 1, Appli
25	918	61.1	1540	3	US-09-967-376-1	Sequence 1, Appli
26	918	61.1	1542	2	US-08-114-695A-1	Sequence 1, Appli
27	914.8	60.9	1542	2	US-08-757-653-158	Sequence 158, App
28	914.8	60.9	1542	3	US-09-465-355-2	Sequence 2, Appli
29	914.8	60.9	1542	3	US-08-520-946-158	Sequence 158, App
30	914.8	60.9	1542	3	US-09-655-378A-158	Sequence 158, App
31	914.8	60.9	1542	3	US-09-548-998E-33	Sequence 33, Appl
32	914.8	60.9	1542	3	US-10-061-071-33	Sequence 33, Appl
33	913	60.8	1830121	3	US-09-557-884-1	Sequence 1, Appli
34	913	60.8	1830121	3	US-09-643-990A-1	Sequence 1, Appli
35	913	60.8	1830121	3	US-10-158-865-1	Sequence 1, Appli
36	911.4	60.7	1487	3	US-09-726-774-14	Sequence 14, Appl
37	907.4	60.4	1449	3	US-09-602-417-1	Sequence 1, Appli
38	907	60.4	1549	3	US-09-492-709A-89	Sequence 89, Appl
39	907	60.4	1549	3	US-09-492-709A-242	Sequence 242, App
40	907	60.4	1549	3	US-09-492-709A-402	Sequence 402, App
c 41	905.8	60.3	1830121	3	US-09-557-884-1	Sequence 1, Appli
c 42	905.8	60.3	1830121	3	US-09-643-990A-1	Sequence 1, Appli
c 43	905.8	60.3	1830121	3	US-10-158-865-1	Sequence 1, Appli
44	904.8	60.2	640681	3	US-09-790-988-1	Sequence 1, Appli
45	903.2	60.1	1541	3	US-09-726-774-2	Sequence 2, Appli

Attachment

ALIGNMENTS

RESULT 1

US-08-632-470-53

; Sequence 53, Application US/08632470

; Patent No. 5976791

; GENERAL INFORMATION:

; APPLICANT: MABILAT, CLAUDE

; APPLICANT: RAOULT, DIDIER

; TITLE OF INVENTION: NUCLEOTIDE FRAGMENTS CAPABLE OF

; TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RRNA AND

; TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS

; NUMBER OF SEQUENCES: 53

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OLIFF & BERRIDGE

; STREET: P.O. BOX 19928

; CITY: ALEXANDRIA

; STATE: VA

; COUNTRY: USA

; ZIP: 22320

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/632,470

; FILING DATE: 08-JUL-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: BERRIDGE, WILLIAM P

; REGISTRATION NUMBER: 30,024

; REFERENCE/DOCKET NUMBER: WPB 38238

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)-836-6400

; TELEFAX: (703)-836-2787

; INFORMATION FOR SEQ ID NO: 53:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1484 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-632-470-53

Query Match 66.2%; Score 994.6; DB 2; Length 1484;

Best Local Similarity 82.5%; Pred. No. 0;

Matches 1194; Conservative 0; Mismatches 245; Indels 9; Gaps 5;

Qy	18	TGCTTAACACATGCAAGTCGAACGGTAACATAATAATGTTTTTACATTTATGGATGAC	77
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Db	100	GAGTGGCGGACGGGTGAGTAATGCGTAGGAATCTACCTTGTAGTGGGGGATAACCTGGGG	159
Qy	138	AAACTACTGGTAATACCGCATGATACTTTAGAGTTAAACTAGCTGAATTTTATAGCTTG	197
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Qy	198	TGCTAAAAGACGGGCTGCGTTAGATTAGCTTGTGGTAAGGTAACGGCTTACCAAGGCA	257
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Qy	258	ACGATCTATAGCTGTTCTGAGAGGAAGATCAGCCACACTGGGACTGAGATACGGCCCA	317
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Qy	318	CTCCTACGGGAGGAGCAGTGGGGAATATTGGACAATGGGCGGAAGCCTGATCCAGCAAT	377
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Qy	378	GCCACGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTTTTATTAGCGAAGAAGATATA	437
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Qy	438	ATGGTTAAGAGCTTAATATATTGACGTTAGCTAAAGAAAAAGCACCAGGCTAACTCCGTG	497
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Qy	498	CCAGCAGCCGCGTAATACGAGGGTGCAAGCGTTAATCGGAATTATTGGGCGTAAAGAG	557
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Qy	558	CCTGTAGGTGGATAATTAAGTCAGATGTGAATCCCAAAGCTTAACCTTGGAACTGCATT	617
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Qy	618	TGAACTAATATCTAGAGTATAGTAGAGGGTAGAGGAATTTCCGGTGTAGCGTGAAAT	677
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Qy	678	CGGTAGAGATCGGAAGGAACATCAGTGGCGAAGCGCTCTACCTGGGACTAAAACAGAC	737
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Qy	738	TGAGAGCGGAAAGCATGGGGAGCAAAACAGGATTAGATACCTGGTAGTCCATGCCGTAAA	797
Db	757	TGAGCGCGGAAAGCATGGGGAGCAAAACAGGATTAGAGACCCTGGTAGTCCACGCGTCAA	816
Qy	798	CTATGAGTACTAAGTGTGGAATTTTAAATTTTAGTAGTGGAGCTAACGCAATAAGTAC	857
Db	817	CGATGAGAACTAGCTGTGGGAAGTTCCTTCTTAGTAGCGAAGCTAACGCGTTAAGTTC	876
Qy	858	TCCGCTGGGGATTACGGCCGCAAGGCTAAAGCAATTTGACGGGGCCCGCACA	917
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Qy	918	AGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAAAACCTTACCTACTCTGAAAT	977
Db	937	AGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAAAACCTTACCTACCTTGACAT	996
Qy	978	CCTTCGTACTTTATAGAGATATAAAGTGCCTT- TGGAACGAAGTGACAGGTGCTGCATG	1036
Db	997	CCTCGGAACCTGTGAGAGATGATTGGTGCCTTCGGGAACCGAGTGACAGGTGCTGCATG	1056
Qy	1037	GCTGTCGTGACGTGCTGTCGTGAGATGTTGGGTTAAGTCCCGTAACGAGCGCAACCCCTT	1096
Db	1057	GCTGTCGTGACGTGCTGTCGTGAGATGTTGGGTTAAGTCCCGTAACGAGCGCAACCCCTG	1116
Qy	1097	CCCTTAGTTGCCAGCGTGTAAAGACGGGACTCTGAGGGGACTGCCGGTGATAAACCGGA	1156
Db	1117	TCCTTAGTTGCCAGCGAGTCAAGTCGGGAACCTAAGGAGACTGCCGGTGATAAACCGGA	1176
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Qy	1217	CAATGGTATGTACAAAGGGAGGCAAAATGTAAAATCTAGCAATCCCAAAAGCATATC	1276
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Db	1297	GTAGTCCGATTGGAGTCTGCAACTCGACTTCATGAAGTTGGAATCGCTAGTAATCGCGA	1356
Qy	1337	ATCAGCATGTGCGGGTGAATACGTTCCCGGGCCCTGTACACACCGCCGTCACACCATGG	1396
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Result 2
US-09-126-774-4

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19	1011.2	67.3	1527	15	AF152597	AF152597 Methyloba
20	1011	67.3	1499	15	AY007296	AY007296 Methylosa
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22	1010.2	67.3	1503	1	DQ270612	DQ270612 Unculture
23	1010	67.2	1536	1	AY662000	AY662000 Unculture
24	1010	67.2	1536	1	AY957925	AY957925 Unculture
25	1009.8	67.2	1486	15	AY744776	AY744776 Legionell
26	1009.8	67.2	1500	1	AB015250	AB015250 Unculture
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28	1009.4	67.2	1499	15	AY007295	AY007295 Methyloba
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c 35	1006.8	67.0	110000	15	CR628337_30	Continuation (31 o
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GenEtbl
Database

ALIGNMENTS

RESULT 1

AY054370

LOCUS AY054370 1502 bp DNA linear ENV 29-APR-2004

DEFINITION Uncultured gamma proteobacterium 16S ribosomal RNA gene, partial sequence.

ACCESSION AY054370

VERSION AY054370.1 GI:29690386

KEYWORDS ENV.

SOURCE uncultured gamma proteobacterium

ORGANISM uncultured gamma proteobacterium
Bacteria; Proteobacteria; Gammaproteobacteria; environmental samples.

REFERENCE 1 (bases 1 to 1502).

AUTHORS Moss, C., Green, D.H., Perez, B., Velasco, A., Henriquez, R. and McKenzie, J.D.

TITLE Intracellular bacteria associated with the ascidian Ecteinascidia turbinata: Phylogenetic and in situ hybridisation analysis

JOURNAL Mar. Biol. 143, 99-110 (2003)

REFERENCE 2 (bases 1 to 1502)

AUTHORS Perez, B., Velasco, A., Henriquez, R. and Sanchez-Puelles, J.M.

TITLE Marine bacteria 16S rRNA gene from a Mediterranean ascidian

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 1502)

AUTHORS Perez, B., Velasco, A., Henriquez, R. and Sanchez-Puelles, J.M.

TITLE Direct Submission

JOURNAL Submitted (30-AUG-2001) Biotechnology, Pharma Mar S.A., c/Calera 3, Tres Cantos, Madrid 28760, Spain

FEATURES Location/Qualifiers

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1..1502

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/specific_host="Ecteinascidia turbinata"

/db_xref="taxon:86473"

/environmental_sample

rRNA

<1..>1502

/product="16S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 1502; DB 1; Length 1502;

Best Local Similarity 100.0%; Pred. No. 1.2;

Matches 1502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61 TTACATTTATGGATGACGAGTGGCGGACGGGTGAGTAACGCGTAGGAACCTACCTTTTAG 120
Db     61 TTACATTTATGGATGACGAGTGGCGGACGGGTGAGTAACGCGTAGGAACCTACCTTTTAG 120

Qy    121 TGGGGGATAGCAGTGGGAAACTACTGGTAATACCGCATGATACTTTAGAGTTAAACTAG 180
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```

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Qy	421	TTAGCGAAGAAGATATAATGGTTAAGAGCTTAATATATTGACGTTAGCTAAAGAAAAAG	480
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Db	481	CACCGGCTAACTCCGTGCCAGCAGCCGCGTAATACGAGGGTGCAAGCGTTAATCGGAA	540
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Db	781	GTAGTCCATGCCGTAAACCTATGAGTACTAACTGTTGGAATTTTAAATTTTAGTAGTGA	840
Qy	841	GCTAACGCAATAAGTACTCCGCTGGGATTACGGCCGCAAGGCTAAAACCTAAAGGAAT	900
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Qy	901	TGACGGGGGGCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCAAAAACC	960
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Db	961	TTACCTACTCTTGAAATCCTTCGTACTTTATAGAGATATAAAGGTGCCTTTGGAACGAAG	1020
Qy	1021	TGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTGAGATGTTGGGTTAAGTCCCGTA	1080
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Qy	1321	TCGCTAGTAATCGCGAATCAGCATGTCGCGGTGAATACGTTCCCGGGCCTTGACACACC	1380
Db	1321	TCGCTAGTAATCGCGAATCAGCATGTCGCGGTGAATACGTTCCCGGGCCTTGACACACC	1380
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Qy	1441	GGTCCCTACGGTGTGTTTCGTAACTGGGGTGAAGTCGTAAACAGGTAGCCGTAGGGAACT	1500
Db	1441	GGTCCCTACGGTGTGTTTCGTAACTGGGGTGAAGTCGTAAACAGGTAGCCGTAGGGAACT	1500
Qy	1501	GC 1502	
Db	1501	GC 1502	

10/524'52

=> d his

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FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS, LIFESCI' ENTERED AT 10:12:22 ON 12 SEP 2006

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L3 1 S GAMMA (A) PROTOBACTERIUM
L4 6 S GAMMA (A) PROTOBACTERI?
L5 0 S 16S(W) RIBOSOMAL (W)RNA
L6 13711 S 16S(W) RIBOSOMAL (W)RNA
L7 85 S PROTOBACTERI?
L8 6 S L6 AND L7
L9 6 DUP REM L8 (0 DUPLICATES REMOVED)
L10 429 S ECTEINASCIDIA (W) TURBINATA
L11 1 S L6 AND L10
L12 6 S CANDIDATUS (W) ENDOECTEINASCIDIA (W) FRUMENTENSIS
L13 1 S L6 AND L12
E ESTEBAN P E/AU
E PEREZ T A/AU
L14 578 S E2
E IGLESIS A V/AU
E MORENO R M/AU
L15 47 S E3
L16 625 S L14 OR L15
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L18 0 S L6 AND L17
L19 0 S L6 AND L16
L20 0 S L12 AND L16

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NEWS 13 JUL 14 FSTA enhanced with Japanese patents
NEWS 14 JUL 19 Coverage of Research Disclosure reinstated in DWPI
NEWS 15 AUG 09 INSPEC enhanced with 1898-1968 archive
NEWS 16 AUG 28 ADISCTI Reloaded and Enhanced
NEWS 17 AUG 30 CA(SM)/CAPplus(SM) Austrian patent law changes
NEWS 18 SEP 11 CA/CAPplus enhanced with more pre-1907 records

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MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
AND CURRENT DISCOVER FILE IS DATED 26 JUNE 2006.

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=> s gamma (a) protobacterium
L3 1 GAMMA (A) PROTOBACTERIUM

=> s gamma (a) protobacteri?
L4 6 GAMMA (A) PROTOBACTERI?

=> s 16S(w) ribozomal (w)RNA
L5 0 16S(W) RIBOZOMAL (W) RNA

=> s 16S(w) ribosomal (w)RNA
L6 13711 16S(W) RIBOSOMAL (W) RNA

=> s protobacteri?
L7 85 PROTOBACTERI?

=> s 16 and 17
L8 6 L6 AND L7

=> dup rem 18
PROCESSING COMPLETED FOR L8
L9 6 DUP REM L8 (0 DUPLICATES REMOVED)

=> d 1-6 ibib ab

L9 ANSWER 1 OF 6 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 2006:148843 BIOSIS
DOCUMENT NUMBER: PREV200600150476
TITLE: Microbial community dynamics during start-up of
bio-hydrogen producing reactor.

AUTHOR(S): Ren, N. Q. [Reprint Author]; Xing, D. F.; Gong, M. L.; Li, Q. B.

CORPORATE SOURCE: Harbin Inst Technol, Sch Municipal and Environm Engrn, Harbin 150090, Peoples R China
rng@hti.edu.cn; ixdf@yahoo.com.cn

SOURCE: Wang, XC [Editor]; Chen, R [Editor]. (2005) pp. 161-168.
Future of Urban Wastewater Systems - Decentralisation and Reuse.
Publisher: CHINA ARCHITECTURE & BUILDING PRESS,
BAIWANZHUANG XICHENGGU, BEIJING, 10037, PEOPLES R CHINA.
Meeting Info.: Conference of the International-Water-Association (IWA). Xian, PEOPLES R CHINA. May 18 -20, 2005.
Xian Univ Architecture & Technol; Int Water Assoc.
ISBN: 7-112-07386-3(S).

DOCUMENT TYPE: Book; (Book Chapter)
Conference; (Meeting)

LANGUAGE: English

ENTRY DATE: Entered STN: 1 Mar 2006
Last Updated on STN: 1 Mar 2006

AB A laboratory-scale continuous hydrogen production is carried on by using molasses as its feed. During these 35 days of the start-up period, microbial community dynamics are monitored by using the denaturing gradient gel electrophoresis (DGGE) analysis of the V3 region of 16S rRNA genes. After running 7-14 days, there is an obvious change in the dominant populations of the microbial community. And this change accompanies with a change of fermentation type. The dominant populations are as follows low G+C gram-positive bacteria, Bacteroides, Actinobacteria and γ -Proteobacteria, respectively. Most of the hydrogen producing bacteria are Clostridium sp., Bacteroides sp., Acetanaerobacterium sp., Megasphaera sp., Bacteroides sp., and Enterobacter sp., respectively. The community structure composition and the amount of dominant population are different when the reactor operates in different periods. Different niche conditions lead to different enrichment of bacteria, and forms different microbial community structures.

L9 ANSWER 2 OF 6 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN

ACCESSION NUMBER: 2005:225133 BIOSIS

DOCUMENT NUMBER: PREV200510010159

TITLE: Coexistence of bacterial sulfide oxidizers, sulfate reducers, and spirochetes in a gutless worm (Oligochaeta) from the Peru margin.

AUTHOR(S): Blazejak, Anna; Erseus, Christer; Amann, Rudolf; Dubilier, Nicole [Reprint Author]

CORPORATE SOURCE: Max Planck Inst Marine Microbiol, Celsiusstr 1, D-28359 Bremen, Germany
ndubilie@mpi-bremen.de

SOURCE: Applied and Environmental Microbiology, (MAR 2005) Vol. 71, No. 3, pp. 1553-1561.
CODEN: AEMIDF. ISSN: 0099-2240.

DOCUMENT TYPE: Article

LANGUAGE: English

ENTRY DATE: Entered STN: 16 Jun 2005
Last Updated on STN: 16 Jun 2005

AB *Olavius crassitunicatus* is a small symbiont-bearing worm that occurs at high abundance in oxygen-deficient sediments in the East Pacific Ocean. Using comparative 16S rRNA sequence analysis and fluorescence in situ hybridization, we examined the diversity and phylogeny of bacterial symbionts in two geographically distant *O. crassitunicatus* populations (separated by 385 km) on the Peru margin (water depth, similar to 300 m). Five distinct bacterial phylotypes co-occurred in all specimens from both sites: two members of the gamma-Proteobacteria (Gamma 1 and 2 symbionts), two members of the delta-Proteobacteria (Delta 1 and 2 symbionts), and one spirochete. A sixth phylotype belonging to the delta-Proteobacteria (Delta 3 symbiont) was found in only one of the two host populations.

Three of the *O. crassitunicatus* bacterial phylotypes are closely related to symbionts of other gutless oligochaete species; the Gamma 1 phylotype is closely related to sulfide-oxidizing symbionts of *Olavius algarvensis*, *Olavius loisae*, and *Inanidrillus leukodermatus*, the Delta 1 phylotype is closely related to sulfate-reducing symbionts of *O. algarvensis*, and the spirochete is closely related to spirochetal symbionts of *O. loisae*. In contrast, the Gamma 2 phylotype and the Delta 2 and 3 phylotypes belong to novel lineages that are not related to other bacterial symbionts. Such a phylogenetically diverse yet highly specific and stable association in which multiple bacterial phylotypes coexist within a single host has not been described previously for marine invertebrates.

L9 ANSWER 3 OF 6 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
 ACCESSION NUMBER: 2005:253069 BIOSIS
 DOCUMENT NUMBER: PREV200510037051
 TITLE: Bacterial community shift along a subsurface geothermal water stream in a Japanese gold mine.
 AUTHOR(S): Hirayama, Hisako [Reprint Author]; Takai, Ken; Inagaki, Fumio; Yamato, Yu; Suzuki, Masae; Nealson, Kenneth H.; Horikoshi, Koki
 CORPORATE SOURCE: Japan Agcy Marine Earth Sci and Technol, Extremobiosphere Res Ctr, Subground Animalcule Retrieval SUGAR Project, 2-15 Natsushima Cho, Yokosuka, Kanagawa 2370061, Japan
 SOURCE: hirayamah@jamstec.go.jp
 SOURCE: Extremophiles, (APR 2005) Vol. 9, No. 2, pp. 169-184.
 ISSN: 1431-0651.
 DOCUMENT TYPE: Article
 LANGUAGE: English
 ENTRY DATE: Entered STN: 8 Jul 2005
 Last Updated on STN: 8 Jul 2005

AB Change of bacterial community occurring along a hot water stream in the Hishikari gold mine, Japan, was investigated by applying a combination of various culture-independent techniques. The stream, which is derived from a subsurface anaerobic aquifer containing plentiful CO₂, CH₄, H₂, and NH₄⁺, emerges in a mine tunnel 320 m below the surface providing nutrients for a lush microbial community that extends to a distance of approximately 7 m in the absence of sunlight-irradiation. Over this distance, the temperature decreases from 69 degrees C to 55 degrees C, and the oxidation-reduction potential increases from -130 mV to +59 mV. In the hot upper reaches of the stream, the dominant phylotypes were: 1) a deeply branching lineage of thermophilic methane-oxidizing gamma-Proteobacteria, and 2) a thermophilic hydrogen- and sulfur-oxidizing *Sulfurihydrogenibium* sp. In contrast, the prevailing phylotypes in the middle and lower parts of the stream were closely related to ammonia-oxidizing *Nitrosomonas* and nitrite-oxidizing *Nitrospira* spp.. Changes in the microbial metabolic potential estimated by competitive PCR analysis of genes encoding the enzymes, particulate methane monooxygenase (*pmoA*), ammonia monooxygenase (*amoA*), and putative nitrite oxidoreductase (*norB*), also substantiated the community shift indicated by 16S rRNA gene analysis. The diversity of putative *norB* lineages was assessed for the first time in the hot water environment. Estimation of dominant phylotypes by whole-cell fluorescent in situ hybridization and changes in inorganic nitrogen compounds such as decreasing ammonium and increasing nitrite and nitrate in the mat-interstitial water along the stream were consistent with the observed transition of the bacterial community structure in the stream.

L9 ANSWER 4 OF 6 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
 ACCESSION NUMBER: 2002:475652 BIOSIS
 DOCUMENT NUMBER: PREV200200475652
 TITLE: Marine nematodes as hosts for chemoautotrophic symbionts.
 AUTHOR(S): Ott, Joerg [Reprint author]; Bright, Monika [Reprint author]; Nussbaumer, Andrea [Reprint author]; Vanura, Katrina; Eichinger, Irmgard [Reprint author]; Schabussova, Irma [Reprint author]

CORPORATE SOURCE: Institute of Ecology and Conservation Biology, University of Vienna, Althanstrasse 14, A-1090, Vienna, Austria
joerg.ott@univie.ac.at

SOURCE: Nematology, (2002) Vol. 4, No. 2, pp. 187-188. print.
Meeting Info.: Fourth International Congress of Nematology
Programme and Abstracts. Tenerife, Canary Islands, Spain.
June 08-13, 2002.
ISSN: 1388-5545.

DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)

LANGUAGE: English

ENTRY DATE: Entered STN: 11 Sep 2002
Last Updated on STN: 11 Sep 2002

L9 ANSWER 5 OF 6 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN

ACCESSION NUMBER: 1999:126171 BIOSIS

DOCUMENT NUMBER: PREV199900126171

TITLE: Bacteria of the genus *Roseobacter* associated with the toxic dinoflagellate *Prorocentrum lima*.

AUTHOR(S): Prokic, Ivo; Bruemmer, Franz; Brigge, Theo; Goertz, Hans D.; Gerdtz, Gunnar; Schuett, Christian; Elbraechter, Malte; Mueller, Werner E. G. [Reprint author]

CORPORATE SOURCE: Inst. Physiol. Chem., Abt. Angewandte Mol., Univ., Duesbergweg 6, D-55099 Mainz, Germany

SOURCE: Protist, (Dec., 1998) Vol. 149, No. 4, pp. 347-357. print.
ISSN: 1434-4610.

DOCUMENT TYPE: Article

LANGUAGE: English

ENTRY DATE: Entered STN: 17 Mar 1999
Last Updated on STN: 17 Mar 1999

AB The dinoflagellate *Prorocentrum lima* is known to produce diarrhetic shellfish poisons. However, it is yet unclear if the dinoflagellates themselves or the bacteria associated with them produce the toxins. Here we analyze the toxicity as well as the spectrum of bacteria in two cultures of *P. lima*, namely *P. lima*-SY and *P. lima*-ST, which initially derived from the same *P. lima* strain PL2V. Toxicity tests, applying the *Artemia* bioassay revealed in both cultures high levels of toxins. The bacteria, associated with the two cultures, were identified by PCR/nucleotide sequence analysis of the 16S rRNA gene. From cultures of *P. lima*-SY the dominant sequence was found to share a 93.7% similarity with the sequence of *Roseobacter algicola* (*R. algicola*); the relative abundance was determined to be 83%. In addition three further sequences of bacteria, grouped to the alpha-Protobacteria have been identified: *Paracoccus denitrificans* (90.8%), *R. algicola* (94.4%) and *Rhizobium huakuii* (92.6%). The identification of bacteria in *P. lima*-ST revealed that most share highest similarity with *Bartonella taylorii* but with a relatively low score of 87%. In addition to this sequence, two sequences with high similarity to the genus *Roseobacter* were obtained. The other sequences identified have not been detected in *P. lima*-SY. Studies with pure bacterial strains, previously isolated from a culture of *P. lima*-ST and subsequently cultured on agar plates, revealed that none of them was identical to those identified in the dinoflagellate culture itself. An explanation for the change of the spectrum of bacteria in the different cultures can only be expected when axenic cultures from *P. lima* are available.

L9 ANSWER 6 OF 6 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN

ACCESSION NUMBER: 1998:313104 BIOSIS

DOCUMENT NUMBER: PREV199800313104

TITLE: *Alcanivorax borkumensis* gen. nov., sp. nov., a new, hydrocarbon-degrading and surfactant-producing marine bacterium.

AUTHOR(S): Yakimov, Michail M.; Golyshin, Peter N. [Reprint author]; Lang, Siegmund; Moore, Edward R. B.; Abraham, Wolf-Rainer;

CORPORATE SOURCE: Luensdorf, Heinrich; Timmis, Kenneth N.
 Div. Microbiol., GBF Natl. Res., Cent. Biotechnol.,
 Mascheroder Weg 1, D-38124 Braunschweig, Germany
 SOURCE: International Journal of Systematic Bacteriology, (April,
 1998) Vol. 48, No. 2, pp. 339-348. print.
 CODEN: IJSBA8. ISSN: 0020-7713.
 DOCUMENT TYPE: Article
 LANGUAGE: English
 ENTRY DATE: Entered STN: 22 Jul 1998
 Last Updated on STN: 22 Jul 1998

AB During screening for biosurfactant-producing, n-alkane-degrading marine bacteria, six heterotrophic bacterial strains were isolated from enriched mixed cultures, obtained from sea water/sediment samples collected near the Isle of Borkum (North Sea), using Mihagol-S (C14,15-n-alkanes) as principal carbon source. These Gram-negative, aerobic, rod-shaped bacteria use a limited number of organic compounds, including aliphatic hydrocarbons, volatile fatty acids, and pyruvate and its methyl ether. During cultivation on n-alkanes as sole source of carbon and energy, all strains produced both extracellular and cell-bound surface-active glucose lipids which reduced the surface tension of water from 72 to 29 mN m⁻¹ (16). This novel class of glycolipids was found to be produced only by these strains. The 16S rRNA gene sequence analysis showed that these strains are all members of the gamma-subclass of the Proteobacteria. Their phospholipid ester-linked fatty acid composition was shown to be similar to that of members of the genus Halomonas, although they did not demonstrate a close phylogenetic relationship to any previously described species. On the basis of the information summarized above, a new genus and species, *Alcanivorax borkumensis*, is described to include these bacteria. Strain SK2T is the type strain of *A. borkumensis*.

=> d his

(FILE 'HOME' ENTERED AT 10:11:52 ON 12 SEP 2006)

FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS,
 LIFESCI' ENTERED AT 10:12:22 ON 12 SEP 2006

L1 0 S S GAMMA (A) PROTOBACTERIUM
 L2 0 S S GAMMA (A) PROTOBACTERI?
 L3 1 S GAMMA (A) PROTOBACTERIUM
 L4 6 S GAMMA (A) PROTOBACTERI?
 L5 0 S 16S(W) RIBOSOMAL (W)RNA
 L6 13711 S 16S(W) RIBOSOMAL (W)RNA
 L7 85 S PROTOBACTERI?
 L8 6 S L6 AND L7
 L9 6 DUP REM L8 (0 DUPLICATES REMOVED)

=> s ecteinascidia (w) turbinata
 L10 429 ECTEINASCIDIA (W) TURBINATA

=> s 16 and l10
 L11 1 L6 AND L10

=> d all

L11 ANSWER 1 OF 1 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
 AN 2003:455344 BIOSIS
 DN PREV200300455344
 TI Intracellular bacteria associated with the ascidian *Ecteinascidia*
 turbinata: Phylogenetic and in situ hybridisation analysis.
 AU Moss, C. [Reprint Author]; Green, D. H.; Perez, B.; Velasco, A.;
 Henriquez, R.; McKenzie, J. D.
 CS Marine Resource Centre, Integrin Advanced Biosystems, Barcaldine, Oban,
 Argyll, PA37 1SE, UK

claire_moss@yahoo.com
 SO Marine Biology (Berlin), (July 2003) Vol. 143, No. 1, pp. 99-110. print.
 CODEN: MBIOAJ. ISSN: 0025-3162.
 DT Article
 LA English
 ED Entered STN: 1 Oct 2003
 Last Updated on STN: 1 Oct 2003
 AB The ascidian *Ecteinascidia turbinata* (Herdman) is a colonial sea squirt found in the Caribbean and Mediterranean Seas. In the present study, the bacterial complement of *E. turbinata* has been assessed by 16S rRNA gene analysis and the most commonly occurring strains identified by restriction fragment length polymorphism. Three strains were found to predominate using this approach, with one representing >50% of clones from both larval and adult material. The 16S rRNA gene sequence of the most commonly occurring strain did not match with any known bacterial sequences and could only be assigned to the gamma-proteobacteria subdivision. The two other frequently occurring strains were assigned to the Mollicutes. In situ hybridisation analysis with eubacterial probes to 16S rRNA revealed the presence of apparently endosymbiotic bacteria in adult and larval tissue, and electron microscopy confirmed the presence of putative bacteriocytes in the larval tissue. The presence of the same bacteria in the brooded larvae suggested that they were vertically transmitted from parent to offspring. Further hybridisation using a novel probe designed to be specific to the 16S rRNA sequence of the dominant strain, highlighted the same cell types as that revealed by the eubacterial probe. The results suggest that the bacteria represent a novel strain, denoted "*Candidatus Endoecteinascidia frumentensis*", and that they may have an important role in the biology of *E. turbinata*.
 CC Ecology: environmental biology - Animal 07508
 Ecology: environmental biology - Oceanography 07512
 IT Major Concepts
 Marine Ecology (Ecology, Environmental Sciences)
 IT Chemicals & Biochemicals
 16S ribosomal RNA
 IT Methods & Equipment
 in situ hybridization analysis: laboratory techniques; phylogenetic analysis: mathematical and computer techniques
 GT Caribbean (West Indies, Neotropical region); Mediterranean Sea (North Atlantic, Atlantic Ocean)
 ORGN Classifier
 Urochordata 85104
 Super Taxa
 Protochordata; Chordata; Animalia
 Organism Name
 Ecteinascidia turbinata (species)
 Taxa Notes
 Animals, Chordates, Invertebrates, Protochordates

=> s candidatus (w) endoecteinascidia (w) frumentensis
 L12 6 CANDIDATUS (W) ENDOECTEINASCIDIA (W) FRUMENTENSIS

=> d his

(FILE 'HOME' ENTERED AT 10:11:52 ON 12 SEP 2006)

FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS, LIFESCI' ENTERED AT 10:12:22 ON 12 SEP 2006

L1 0 S S GAMMA (A) PROTOBACTERIUM
 L2 0 S S GAMMA (A) PROTOBACTERI?
 L3 1 S GAMMA (A) PROTOBACTERIUM
 L4 6 S GAMMA (A) PROTOBACTERI?
 L5 0 S 16S(W) RIBOSOMAL (W)RNA
 L6 13711 S 16S(W) RIBOSOMAL (W)RNA

L7 85 S PROTOBACTERI?
 L8 6 S L6 AND L7
 L9 6 DUP REM L8 (0 DUPLICATES REMOVED)
 L10 429 S ECTEINASCIDIA (W) TURBINATA
 L11 1 S L6 AND L10
 L12 6 S CANDIDATUS (W) ENDOECTEINASCIDIA (W) FRUMENTENSIS

=> s l6 and l12

L13 1 L6 AND L12

=> d ibib ab

L13 ANSWER 1 OF 1 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
 ACCESSION NUMBER: 2003:455344 BIOSIS
 DOCUMENT NUMBER: PREV200300455344
 TITLE: Intracellular bacteria associated with the ascidian
 Ecteinascidia turbinata: Phylogenetic and in situ
 hybridisation analysis.
 AUTHOR(S): Moss, C. [Reprint Author]; Green, D. H.; Perez, B.;
 Velasco, A.; Henriquez, R.; McKenzie, J. D.
 CORPORATE SOURCE: Marine Resource Centre, Integrin Advanced Biosystems,
 Barcaldine, Oban, Argyll, PA37 1SE, UK
 claire_moss@yahoo.com
 SOURCE: Marine Biology (Berlin), (July 2003) Vol. 143, No. 1, pp.
 99-110. print.
 CODEN: MBIOAJ. ISSN: 0025-3162.
 DOCUMENT TYPE: Article
 LANGUAGE: English
 ENTRY DATE: Entered STN: 1 Oct 2003
 Last Updated on STN: 1 Oct 2003

AB The ascidian Ecteinascidia turbinata (Herdman) is a colonial sea squirt found in the Caribbean and Mediterranean Seas. In the present study, the bacterial complement of E. turbinata has been assessed by 16S rRNA gene analysis and the most commonly occurring strains identified by restriction fragment length polymorphism. Three strains were found to predominate using this approach, with one representing >50% of clones from both larval and adult material. The 16S rRNA gene sequence of the most commonly occurring strain did not match with any known bacterial sequences and could only be assigned to the gamma-proteobacteria subdivision. The two other frequently occurring strains were assigned to the Mollicutes. In situ hybridisation analysis with eubacterial probes to 16S rRNA revealed the presence of apparently endosymbiotic bacteria in adult and larval tissue, and electron microscopy confirmed the presence of putative bacteriocytes in the larval tissue. The presence of the same bacteria in the brooded larvae suggested that they were vertically transmitted from parent to offspring. Further hybridisation using a novel probe designed to be specific to the 16S rRNA sequence of the dominant strain, highlighted the same cell types as that revealed by the eubacterial probe. The results suggest that the bacteria represent a novel strain, denoted "Candidatus Endoecteinascidia frumentensis", and that they may have an important role in the biology of E. turbinata.

=> d his

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 L7 85 S PROTOBACTERI?
 L8 6 S L6 AND L7
 L9 6 DUP REM L8 (0 DUPLICATES REMOVED)
 L10 429 S ECTEINASCIDIA (W) TURBINATA
 L11 1 S L6 AND L10
 L12 6 S CANDIDATUS (W) ENDOECTEINASCIDIA (W) FRUMENTENSIS
 L13 1 S L6 AND L12

=> e esteban p e/au

E1 1 ESTEBAN OSVALDO/AU
 E2 50 ESTEBAN P/AU
 E3 0 --> ESTEBAN P E/AU
 E4 26 ESTEBAN P F/AU
 E5 2 ESTEBAN P G/AU
 E6 3 ESTEBAN P L/AU
 E7 1 ESTEBAN P O/AU
 E8 2 ESTEBAN PALACIO J/AU
 E9 2 ESTEBAN PALOMA/AU
 E10 1 ESTEBAN PARGA FRANCISCO JAVIER/AU
 E11 15 ESTEBAN PARRA M J/AU
 E12 1 ESTEBAN PATRICIA/AU

=> e perez t a/au

E1 13 PEREZ SYLVIE/AU
 E2 578 PEREZ T/AU
 E3 4 --> PEREZ T A/AU
 E4 1 PEREZ T A T/AU
 E5 1 PEREZ T ALDEIMA T/AU
 E6 4 PEREZ T B/AU
 E7 1 PEREZ T B STACH/AU
 E8 9 PEREZ T C/AU
 E9 13 PEREZ T D/AU
 E10 32 PEREZ T E/AU
 E11 1 PEREZ T FERNANDEZ/AU
 E12 28 PEREZ T H/AU

=> s e2

L14 578 "PEREZ T"/AU

=> e iglesias a v/au

E1 2 IGLESIASYDELACUEVA C/AU
 E2 1 IGLESIES I ANGLES D JOSEP/AU
 E3 0 --> IGLESIS A V/AU
 E4 1 IGLESIS C/AU
 E5 8 IGLESIS R/AU
 E6 1 IGLESISA M J/AU
 E7 1 IGLESISAS RUBIANES L/AU
 E8 3 IGLESIUS G/AU
 E9 1 IGLESIUS GABRIELA/AU
 E10 1 IGLESIUS ROZAS J R/AU
 E11 1 IGLESKI B/AU
 E12 1 IGLESLAS A/AU

=> e moreno r m/au

E1 1 MORENO R JUAN JOSE/AU
 E2 27 MORENO R L/AU
 E3 47 --> MORENO R M/AU
 E4 15 MORENO R M B/AU
 E5 2 MORENO R M G/AU
 E6 1 MORENO R MA/AU
 E7 1 MORENO R NORALBA/AU
 E8 13 MORENO R O/AU
 E9 19 MORENO R P/AU

E10 1 MORENO R PARADA/AU
E11 1 MORENO R PENA/AU
E12 4 MORENO R R/AU

=> s e3

L15 47 "MORENO R M"/AU

=> d his

(FILE 'HOME' ENTERED AT 10:11:52 ON 12 SEP 2006)

FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS, LIFESCI' ENTERED AT 10:12:22 ON 12 SEP 2006

L1 0 S S GAMMA (A) PROTOBACTERIUM
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L7 85 S PROTOBACTERI?
L8 6 S L6 AND L7
L9 6 DUP REM L8 (0 DUPLICATES REMOVED)
L10 429 S ECTEINASCIDIA (W) TURBINATA
L11 1 S L6 AND L10
L12 6 S CANDIDATUS (W) ENDOECTEINASCIDIA (W) FRUMENTENSIS
L13 1 S L6 AND L12
E ESTEBAN P E/AU
E PEREZ T A/AU
L14 578 S E2
E IGLESIS A V/AU
E MORENO R M/AU
L15 47 S E3

=> s l14 or l15

L16 625 L14 OR L15

=> s l10 and l16

L17 0 L10 AND L16

=> s l6 and l17

L18 0 L6 AND L17

=> s l6 and l16

L19 0 L6 AND L16

=> s l12 and l16

L20 0 L12 AND L16

=> d his

(FILE 'HOME' ENTERED AT 10:11:52 ON 12 SEP 2006)

FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS, LIFESCI' ENTERED AT 10:12:22 ON 12 SEP 2006

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L6 13711 S 16S(W) RIBOSOMAL (W)RNA
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L9 6 DUP REM L8 (0 DUPLICATES REMOVED)
L10 429 S ECTEINASCIDIA (W) TURBINATA

L11	1 S L6 AND L10
L12	6 S CANDIDATUS (W) ENDOECTEINASCIDIA (W) FRUMENTENSIS
L13	1 S L6 AND L12 E ESTEBAN P E/AU E PEREZ T A/AU
L14	578 S E2 E IGLESIS A V/AU E MORENO R M/AU
L15	47 S E3
L16	625 S L14 OR L15
L17	0 S L10 AND L16
L18	0 S L6 AND L17
L19	0 S L6 AND L16
L20	0 S L12 AND L16

	Issue Date	Page s	Document ID	Title
1	20060727	22	US 2006016722 8 A1	Sequences from an endosymbiont and their uses

	Issue Date	Page s	Document ID	Title
1	20060706	72	US 2006014795 8 A1	System for detecting polynucleotides
2	20051110	79	US 2005025020 6 A1	Development of DNA probes and immunological reagents specific for cell surface- expressed molecules and transformation- associated genes
3	20050728	75	US 2005016370 9 A1	Development of DNA probes and immunological reagents specific for cell surface- expressed molecules and transformation- associated genes
4	20020829	119	US 2002012011 6 A1	ENTEROCOCCUS FAECALIS POLYNUCLEOTIDES AND POLYPEPTIDES
5	20041102	73	US 6811972 B1	Development of DNA probes and immunological reagents specific for cell surface- expressed molecules and transformation- associated genes
6	20040420	59	US 6723837 B1	Nucleic acid molecule and encoded protein associated with sterol synthesis and metabolism

	Issue Date	Page s	Document ID	Title
7	20010710	94	US 6258359 B1	Immunogenic compositions against helicobacter infection, polypeptides for use in the compositions, and nucleic acid sequences encoding said polypeptides
8	20010619	94	US 6248330 B1	Immunogenic compositions against helicobacter infection, polypeptides for use in the compositions, and nucleic acid sequences encoding said polypeptides
9	20001226	30	US 6165992 A	Histidine kinase
10	19981201	92	US 5843460 A	Immunogenic compositions against helicobacter infection, polypeptides for use in the compositions, and nucleic acid sequences encoding said polypeptides
11	19970311	16	US 5610060 A	Isolated Helicobacter hepaticus
12	19961210	12	US 5582975 A	Nucleic acid probes to staphylococcus aureus

	L #	Hits	Search Text
1	L1	1	"5976791".pn.
2	L2	26	candidatus
3	L3	0	l1 and l2
4	L4	900	16S adj ribosomal adj RNA
5	L5	51	Ecteinascidia adj turbinata
6	L6	0	l4 same l5
7	L7	1	Candidatus adj endoecteinascidia adj frumentensis
8	L8	1	gamma adj protobacteri\$3
9	L9	1481 0	ESTEBAN IGLESIS MORENO PEREZ
10	L11	0	l5 and l10
11	L10	12	l4 and l9